Table S1. Related to Figure 1. Description of all scRNA-seq datasets used in this study.

Dataset	Citation	GEO/SRA access number	Description of the experiment
Mouse Influenza A	https://www.ncbi.nlm.nih.gov/pubmed/29886109	GSE126042 / SRP126257	Intranasal infection of mouse lung by PR8 H1N1 Influenza A strain. Immune and non immune cells are sequenced 48 or 72h post infection using MARS-seq technology.
Spleen LCMV (NICHE-seq)	https://science.sciencemag.org/content/358/6370/1622.long	GSE104054 / SRP118316	Mice receive LCMV injection in the footpad. 72h later, spleen is harvested and cells from the different spleen regions are sequenced using the NICHE-seq/MARS-seq technology.
Lymph Node LCMV/VSV	NA	NA	Intradermal infection by LCMV and VSV near the ear pinna. Immune non B/T cells from the draining lymph node are sequenced 24h later using MARS-seq technology.
In vitro HSV-1 infection	https://elifesciences.org/articles/46339	GSE126042 / SRP183453	Human fibroblasts were infected in vitro by HSV-1 (Strain 17) and sequenced 5h later using the DROP-seq technology.
In vitro HIV infection	https://www.ncbi.nlm.nih.gov/pmc/articles/PMC6258175/	NA / SRP134859	In vitro infection of human CD4+ T cells by HIV and sequenced 12 weeks post infection by 10X Genomics technology.

COVID-19 patients	https://www.medrxiv.org/content/10.1101/2020.02.23.20026690v1	GSE145926	Broncho Alveolar Lavage of mild and severe COVID-19 patients. Whole cell content is sequenced using 10X Genomics technology.
HBV patients	**NA**	GSE145926	Liver biopsy from an acute HBV patient. Whole cell content is sequenced using 10X Genomics technology

Table S2. Related to Figure 4.
Enrichment of SARS-CoV-2 UMI in different populations across the six severe patients (S1-S6). Values represent subset log2 between observed and expected viral UMI per patient.

	S1	S2	S3	S4	S5	S6
Neutrophils	-0.32	-0.14	-1.55	-0.25	-0.01	0.00
Alveolar Macrophages	-0.06	-0.72	-0.13	NA	-0.01	-0.01
Alveolar Macrophages (MARCO^{lo})	-0.04	-0.64	-0.07	-0.04	0.00	-0.17
Mon-derived mac (SPP1^{hi} C1QA^{lo})	-0.56	-0.24	0.47	0.73	-0.06	-0.07
Mon-derived mac (SPP1^{hi} C1QA^{hi})	1.72	0.35	-0.34	0.87	-0.08	-0.15
Mon-derived mac (IL1B^{hi})	-0.79	-0.16	-0.67	-0.18	0.05	-0.73
Monocytes I	-1.28	0.88	-0.87	-0.15	-0.02	-0.07
Monocytes II	-1.36	-1.56	-0.28	0.32	-0.05	-0.05
Monocytes (IFNA^{hi})	-0.10	-0.02	NA	NA	NA	NA
DC	-0.13	-1.55	-0.27	-0.01	-0.01	-0.01
Plasmacytoid DC (pDC)	0.23	2.39	NA	NA	NA	NA
Mast cells	-0.01	-0.03	NA	-0.11	-0.01	0.00
CD4^{+} T cells	-0.37	-0.69	-0.45	-0.01	-0.01	-0.10
Naive CD4^{+} T cells (CCR7^{hi})	-0.45	-0.29	1.24	-0.02	-0.16	-0.02
T_{regs}	-0.06	-0.10	NA	NA	0.00	-0.01
T_{fh}	-0.14	-0.14	-0.11	NA	0.00	0.00
Effector CD8^{+} T cells	-0.30	-0.80	-0.11	-0.02	-0.10	-0.12
CD8^{+} T_{rm} (ZNF683_{hi})	-0.09	1.00	-0.44	0.00	-0.02	-0.02
Cytotoxic CD8^{+} T cells	-0.29	-0.73	-0.57	-0.12	-0.03	-0.12
NK cells	-0.43	-0.20	-0.07	-0.10	-0.01	-0.03
B cells	-0.02	-0.21	-0.32	-0.01	-0.02	-0.01
Epithelial progenitors	-0.02	0.30	1.12	-0.33	0.00	-0.01
Ciliated cells	-0.14	1.04	-0.64	-0.38	0.18	0.21
Club cells	-0.28	-0.70	-0.59	-0.27	0.24	0.86
Goblet cells	-0.10	-1.70	0.20	-0.62	-0.03	-0.05
Alveolar type 2	-0.20	-0.25	NA	NA	0.00	0.00
Ionocytes	NA	0.29	0.03	0.45	NA	0.00